# RAW SEQUENCE LISTING
# ERROR REPORT
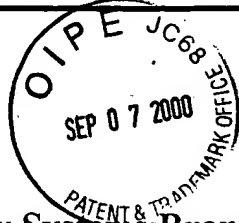
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: *09/548,717*

Art Unit / Team No. : *OIPE*

Date Processed by STIC: *4/28/2000*

## THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

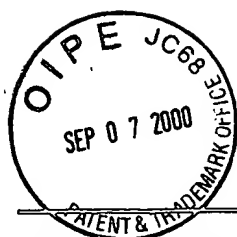IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

# Raw Sequence Listing Error Summary

**ERROR DETECTED** **SUGGESTED CORRECTION** SERIAL NUMBER: _09/548,717_

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 _____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos — The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length — The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering — The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII — This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
**(2) INFORMATION FOR SEQ ID NO:X:**
**(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**
**This sequence is intentionally skipped**

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
**<210> sequence id number**
**<400> sequence id number**
**000**

10 _____ Use of **n's** or **Xaa's** (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 _____ Use of <213>Organism (NEW RULES) — Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES) — Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" — **Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted** file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.
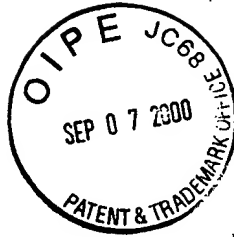
RAW SEQUENCE LISTING
PATENT APPLICATION:  US/09/548,717

DATE: 05/03/2000
TIME: 16:30:47

Input Set : A:\200017.app
Output Set: N:\CRF3\050300\I548717.raw

```
 3 <110> APPLICANT: Toyo Boseki Kabushiki Kaisha
 5 <120> TITLE OF INVENTION: METHOD OF EXTRACTING NUCLEIC ACIDS USING PARTICULATE
 6        CARRIER
 8 <130> FILE REFERENCE: 200017
10 <140> CURRENT APPLICATION NUMBER: US/09/548,717
11 <141> CURRENT FILING DATE: 2000-04-13
13 <160> NUMBER OF SEQ ID NOS: 4
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 24
19 <212> TYPE: DNA
20 <213> ORGANISM: Artificial Sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a
24        sequence complementary to the nucleotides 102
25        through 125 of the nucleotide sequence of V.
26        parahaemolyticus TDH (Thermostable Direct
27        Haemolysin) gene.
29 <400> SEQUENCE: 1
30 ccccggttct gatgagatat tgtt                                    24
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 51
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a
40        sequence complementary to the nucleotides 495-518
41        of the nucleotide seq. of V. parahaemolyticus TDH
42        gene, and a promoter sequence for T7-RNA
43        polymerase.
45 <400> SEQUENCE: 2
46 aattctaata cgactcacta tagggagacc aatatattac cactaccact a          51
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 26
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a
56        sequence complementary to the nucleotides 339
57        through 364 of the nucleotide sequence of V.
58        parahaemolyticus TDH (Thermostable Direct
59        Haemolysin) gene.
61 <400> SEQUENCE: 3
62 cggtcattct gctgtgttcg taaaat                                  26
65 <210> SEQ ID NO: 4
66 <211> LENGTH: 24
67 <212> TYPE: DNA
```

RAW SEQUENCE LISTING                           DATE: 05/03/2000
PATENT APPLICATION: US/09/548,717              TIME: 16:30:47

Input Set : A:\200017.app
Output Set: N:\CRF3\050300\I548717.raw

68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a
72         sequence complementary to the nucleotides 254
73         through 277 of the nucleotide sequence of V.
74         parahaemolyticus TDH (Thermostable Direct
W-GK 75     Haemolysin) gene.
77 <400> SEQUENCE: 4
W--> 78 caggtactaa anggttgaca tcct                                    24

*see item 10 on Error Summary Sheet*

VERIFICATION SUMMARY                          DATE: 05/03/2000
PATENT APPLICATION:  US/09/548,717            TIME: 16:30:48

Input Set : A:\200017.app
Output Set: N:\CRF3\050300\I548717.raw

L:10 M:270 C: Current Application_Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:43 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:59 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:75 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:78 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:78 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:78 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4